

## SEQUENCE LISTING

<110> Ikawa, Yoji  
Otsuka Pharmaceutical Co. Ltd.

<120> Human p53 gene and its product

<130> P99-16

<140>

<141>

<150> JP P1998-100467

<151> 19 98-03-27

<160> 2.3

<170> Patentin Ver. 2.0

<210> 1

<211> 448

<212> PRT

<213> Human

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<221> DOMAIN

<222> (1).. (59)

<223> transactivation domain

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<221> DNA BIND

<222> (142).. (321)

<223> DNA binding domain

<220>

<221> DOMAIN

<222> (353).. (397)

<223> oligomerization domain

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Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro  
20 25 30

Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn  
35 40 45

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu  
50 55 60

Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser  
65 70 75 80

Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn  
85 90 95

Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln  
100 105 110

Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser  
115 120 125

Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln  
130 135 140

Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys  
145 150 155 160

Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val  
165 170 175

Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr

*Sub A1*

2/15

180 185 190  
 Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His  
 195 200 205  
 Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His  
 210 215 220  
 Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro  
 225 230 235 240  
 Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val  
 245 250 255  
 Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser  
 260 265 270  
 Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu  
 275 280 285  
 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg  
 290 295 300  
 Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile  
 305 310 315 320  
 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys  
 325 330 335  
 Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys  
 340 345 350  
 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly  
 355 360 365  
 Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu  
 370 375 380  
 Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln  
 385 390 395 400  
 Gln Gln Gln His Gln His Leu Leu Gln Lys His Leu Leu Ser Ala Cys  
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 435 440 445

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 <222> (2786).. (2791)

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 aaagaaagtt attaccgac cacc atg tcc cag agc aca cag aca aat gaa 171  
 Met Ser Gln Ser Thr Gln Thr Asn Glu

*Handwritten:*  
 mb  
 B1  
 w

180 185 190

Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His  
195 200 205

Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His  
210 215 220

Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro  
225 230 235 240

Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val  
245 250 255

Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser  
260 265 270

Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu  
275 280 285

Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg  
290 295 300

Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile  
305 310 315 320

Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys  
325 330 335

Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys  
340 345 350

Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly  
355 360 365

Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu  
370 375 380

Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln  
385 390 395 400

Gln Gln Gln His Gln His Leu Leu Gln Lys His Leu Leu Ser Ala Cys  
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Phe Arg Asn Glu Leu Val Glu Pro Arg Arg Glu Thr Pro Lys Gln Ser  
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Asp Val Phe Phe Arg His Ser Lys Pro Pro Asn Arg Ser Val Tyr Pro  
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aaagaaggtt attaccgata cacc atg tcc cag agc aca cag aca aat gaa 171  
Met Ser Gln Ser Thr Gln Thr Asn Glu

cga cgc tgc ttt gag gcc cgg atc tgt gct tgc cca gga aga gac aag 1083  
 Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg  
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 aag cgc gat gaa gat agc atc aga aag cag caa gtt tgc gac agt aca 1131  
 Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp Ser Thr  
 315 320 325  
 aag aac ggt gat ggt acg aag cgc cgg ttt cgt cag aac aca cat ggt 1179  
 Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr His Gly  
 330 335 340 345  
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 Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp Glu Leu  
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 tta tac tta cca gtg agt ggc cgt gag act tat gaa atg ctg ttg aag 1275  
 Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu Leu Lys  
 365 370 375  
 atc aaa gag tcc ctg gaa ctg atg cag tac ctt cct cag cac aca att 1323  
 Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His Thr Ile  
 380 385 390  
 gaa acg tac agt caa cag caa cag cag cag cag cag cag tta ctt cag 1371  
 Glu Thr Tyr Arg Gln Gln Gln Gln Gln Gln His Gln His Leu Leu Gln  
 395 400 405  
 aaa cat ctg ctt tca gcc tgc ttc agt aat gag ctt gtg gag ccc cgg 1419  
 Lys His Leu Leu Ser Ala Cys Phe Arg Asn Glu Leu Val Glu Pro Arg  
 410 415 420 425  
 aga gaa act cca aaa caa tct gac gtc ttc ttt aga cat tcc aag ecc 1467  
 Arg Glu Thr Pro Lys Gln Ser Asp Val Phe Phe Arg His Ser Lys Pro  
 430 435 440  
 cca aac cga tca gtg tac cca tagagcccta tctctatatt ttaagtgtgt 1518  
 Pro Asn Arg Ser Val Tyr Pro 445  
 gtgtgtatt tccatgtgta taigtgagt taigtgtgt taigtgtgt cgtgtgtatc 1578  
 tagccctcat aacaggact tgaagacat ttggtcaga gacccaactg ctcaaaggca 1638  
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 tgtaataata ttgcaagtag taagaacga aggtgtcaag tttactgtg ggcagcgagg 2058  
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 ctactacaa aaactgttg ttggcccc atagcaggtg aactcattt gtgttttaa 2298  
 tagaagaca aatccacccc agtaatatg ccttacgta gttgtttacc attaticaa 2358  
 gtcnaaata gaattigaag cctctcaca aaatcgtga ttaatttgt taattagac 2418  
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mb  
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 21

acitctggac tggaaattaa agattguuag ggtagactac tttcttttt ttactcaaa 2598  
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 caatttaaaa atgttccctc cctccattt cccacacca gtcaccagca ctgtatttc 2718  
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 Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn  
 35 40 45  
 Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu  
 50 55 60  
 Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser  
 65 70 75 80  
 Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn  
 85 90 95  
 Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln  
 100 105 110  
 Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser  
 115 120 125  
 Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln  
 130 135 140  
 Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys  
 145 150 155 160  
 Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val  
 165 170 175  
 Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr  
 180 185 190  
 Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His  
 195 200 205  
 Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His  
 210 215 220  
 Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro  
 225 230 235 240  
 Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val  
 245 250 255  
 Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser  
 260 265 270  
 Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu  
 275 280 285  
 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg  
 290 295 300

*Handwritten signature*

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Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile  
305 310 315 320  
Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys  
325 330 335  
Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys  
340 345 350  
Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly  
355 360 365  
Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu  
370 375 380  
Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln  
385 390 395 400  
Gln Gln Gln His Gln His Leu Leu Gln Lys His Leu Leu Ser Ala Cys  
405 410 415  
Phe Arg Asn Glu Leu Val Glu Pro Arg Arg Glu Thr Pro Lys Gln Ser  
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Asp Val Phe Phe Arg His Ser Lys Pro Pro Asn Arg Ser Val Tyr Pro  
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<220>  
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Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn  
35 40 45  
Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu  
50 55 60  
Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser  
65 70 75 80  
Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn  
85 90 95  
Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln  
100 105 110  
Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser  
115 120 125  
Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln

Sub  
A1

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130 135 140

Ser 145 Ser Thr Ala Lys 150 Ser Ala Thr Trp Thr Tyr 155 Ser Thr Glu Leu Lys 160

Lys Leu Tyr Cys Gln 165 Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val 175

Met Thr Pro 180 Pro Gln Gly Ala Val 185 Ile Arg Ala Met Pro Val Tyr 190

Lys Lys Ala 195 Glu His Val Thr Glu Val Val Lys Arg Cys 205 Pro Asn His 210

Glu Leu Ser Arg Glu Phe 215 Asn Glu Gly Gln Ile Ala Pro Pro Ser His 220

Leu Ile Arg Val Glu 230 Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro 240

Ile Thr Gly Arg Glu 245 Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val 255

Gly Thr Glu Phe Thr Thr Val Leu Tyr 265 Asn Phe Met Cys Asn Ser Ser 270

Cys Val Gly Gly Met Asn Arg Arg 280 Pro Ile Leu Ile Ile Val Thr Leu 285

Glu Thr Arg Asp Gly Gln Val 295 Leu Gly Arg Arg Cys Phe Glu Ala Arg 300

Ile Cys Ala Cys Pro 310 Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile 320

Arg Lys Gln Gln Val 325 Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys 335

Arg Pro Phe Arg Gln Asn Thr His 345 Gly Ile Gln Met Thr Ser Ile Lys 350

Lys Arg Arg Ser Pro Asp Asp Glu 360 Leu Leu Tyr Leu Pro Val Arg Gly 365

Arg Glu Thr Tyr Glu Met 375 Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu 380

Met Gln Tyr Leu Pro 380 Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln 395 400

Gln Gln Gln His 405 Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser 415

Pro Ser Ser Tyr 420 Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser 430

Met Asn Lys 435 Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg 445

Asn Ala Leu Thr Pro Thr Thr 455 Ile Pro Asp Gly Met Gly Ala Asn Ile 460

Pro Met Met Gly Thr His 470 Met Pro Met Ala Gly Asp Met Asn Gly Leu 480

Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser Thr Ser 495

His Cys Thr Pro Pro Pro Pro Tyr 505 Pro Thr Asp Cys Ser Ile Val Ser 510

Phe Leu Ala Arg Leu Gly Cys 520 Ser Ser Cys Leu Asp Tyr Phe Thr Thr 525

*One  
81  
m*

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Gln Gly Leu Thr Thr Ile Tyr Gln Ile Glu His Tyr Ser Met Asp Asp  
530 535 540  
Leu Ala Ser Leu Lys Ile Pro Glu Gln Phe Arg His Ala Ile Trp Lys  
545 550 555 560  
Gly Ile Leu Asp His Arg Gln Leu His Glu Phe Ser Ser Pro Ser His  
565 570 575  
Leu Leu Arg Thr Pro Ser Ser Ala Ser Thr Val Ser Val Gly Ser Ser  
580 585 590  
Glu Thr Arg Gly Glu Arg Val Ile Asp Ala Val Arg Phe Thr Leu Arg  
595 600 605  
Gln Thr Ile Ser Phe Pro Pro Arg Asp Glu Trp Asn Asp Phe Asn Phe  
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625 630 635 640  
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aaagaaagtt attaccgntc cacc atg tcc cag agc aca cag aca aat gaa 171  
Met Ser Gln Ser Thr Gln Thr Asn Glu  
1 5  
ttc ctc agt cca gag gtt ttc cag cat atc tgg gat ttt ctg gaa cag 219  
Phe Leu Ser Pro Glu Val Phe Gln His Ile Trp Asp Phe Leu Glu Gln  
10 15 20 25  
cct ata tgt tca gtt cag ccc att gac tgg aac ttt gtc gat gaa cca 267  
Pro Ile Cys Ser Val Gln Pro Ile Asp Leu Asn Phe Val Asp Glu Pro  
30 35 40  
tca gaa gat ggt gcg aca aac gag att gag att agc atg gac tgt atc 315  
Ser Glu Asp Gly Ala Thr Asn Lys Ile Glu Ile Ser Met Asp Cys Ile  
45 50 55  
cgc atg cag gac tgg gac ctg agt gac ccc atg tgg cca cag tac acc 363  
Arg Met Gln Asp Ser Asp Leu Ser Asp Pro Met Trp Pro Gln Tyr Thr  
60 65 70  
aac ctg ggc ctc ctg aac agc atg gac cag cag att cag aac agc tcc 411  
Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn Gly Ser  
75 80 85  
tcg tcc acc agt ccc tat aac aca gac cac gcg cag aac agc gtc acc 459  
Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser Val Thr  
90 95 100 105  
gcg ccc tgg ccc tac gca cag ccc agc tcc acc ttc gat gct ctc tct 507  
Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala Leu Ser  
110 115 120  
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125 130 135

*Handwritten signature*



And  
Ahl

[illegible]

Ans  
A11

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Gln His Ile Trp 20 Asp Phe Leu Glu Gln 25 Pro Ile Cys Ser Val Gln Pro 30

1. The first group of people who are interested in the study of the history of the world are the historians. They are people who study the past and try to understand what happened and why it happened. They use a variety of sources, including books, documents, and artifacts, to reconstruct the past.

Ans. A1

12/15

Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg  
435 440 445  
Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Ile  
450 455 460  
Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp Met Asn Gly Leu  
465 470 475 480  
Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser Thr Ser  
485 490 495  
His Cys Thr Pro Pro Pro Pro Tyr Pro Thr Asp Cys Ser Ile Val Ser  
500 505 510  
Phe Leu Ala Arg Leu Gly Cys Ser Ser Cys Leu Asp Tyr Phe Thr Thr  
515 520 525  
Gln Gly Leu Thr Thr Ile Tyr Gln Ile Glu His Tyr Ser Met Asp Asp  
530 535 540  
Leu Ala Ser Leu Lys Ile Pro Glu Gln Phe Arg His Ala Ile Trp Lys  
545 550 555 560  
Gly Ile Leu Asp His Arg Gln Leu His Glu Phe Ser Ser Pro Ser His  
565 570 575  
Leu Leu Arg Thr Pro Ser Ser Ala Ser Thr Val Ser Val Gly Ser Ser  
580 585 590  
Glu Thr Arg Gly Glu Arg Val Ile Asp Ala Val Arg Phe Thr Leu Arg  
595 600 605  
Gln Thr Ile Ser Phe Pro Pro Arg Asp Glu Trp Asn Asp Phe Asn Phe  
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Glu

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primer

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27

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<220>  
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antisense primer

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<210> 10  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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 <212> DNA  
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<220>  
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 <212> DNA  
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 <223> Description of Artificial Sequence:p51-F2 sense  
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13/15

Handwritten signature/initials.

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19

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 primer

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 antisense primer

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18

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 primer

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19

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 181

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18

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primer

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antisense primer

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and  
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